



#15B

-1-

SEQUENCE LISTING

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<110> Hartley, James L.
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Cheo, David

<120> Compositions and Methods for Use in
Recombinational Cloning of Nucleic Acids

<130> 0942.4680003

<140> 09/517,466

<141> 2000-03-02

E1
<150> US 60/122,389

<151> 1999-03-02

<150> US 60/126,049

<151> 1999-03-23

<150> US 60/136,744

<151> 1999-05-28

<160> 285

<170> PatentIn version 3.1

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ttttacgttt ctggttcagc tttttgtac aaagttggca ttataaaaaa gcattgctca 180
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aatatcaata tattaaatta gatatttgcac aaaaaacaga ctacataata ctgtaaaaca 180
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 cttgtacaaa gtggt 135

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Lys	Lys	Ala	Gly	Phe	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Thr	Met
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<213> B2-Hgb

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<221> gene

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<223> attL1

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<222> (321) .. (626)

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<222> (655) .. (754)

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<222> (877)..(1686)

<223> KmR

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<222> (1791)..(2364)

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<210> 185

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<213> Artificial Sequence

<220>

<223> pENTR1A multiple cloning site

<220>

<221> CDS

<222> (1)..(63)

<223>

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<400> 185
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Thr Leu Tyr Lys Lys Ala Gly Phe Lys Gly Thr Asn Ser Val Asp Trp
1 5 10 15

atc cgg tac cga att c 64
Ile Arg Tyr Arg Ile
20

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<210> 186

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR1A multiple cloning site

<400> 186

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1				5					10					15	

Ile	Arg	Tyr	Arg	Ile
			20	

<210> 187

<211> 49

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<213> Artificial Sequence

<220>

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<400> 187

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49

<210> 188

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR2B multiple cloning site

<220>

<221> CDS

<222> (1)..(60)

<223>

<400> 188

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Leu	Tyr	Lys	Lys	Ala	Gly	Trp	Arg	Arg	Asn	Gln	Phe	Ser	Arg	Leu	Asp
1				5					10					15	

48

ccg	gta	ccg	aat	tc
Pro	Val	Pro	Asn	
			20	

62

<210> 189

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR2B multiple cloning site

<400> 189

Leu	Tyr	Lys	Lys	Ala	Gly	Trp	Arg	Arg	Asn	Gln	Phe	Ser	Arg	Leu	Asp
1				5					10					15	

Pro	Val	Pro	Asn
			20

<210> 190

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR2B multiple cloning site

<220>

<221> CDS

<222> (2)..(49)

<223>

<400> 190

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	Asn	Ser	Arg	Pro	His	Ser	Arg	Tyr	Leu	Asp	Pro	Ala	Phe	Leu	Tyr	Lys	
1					5					10					15		

g																	50
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<210> 191

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR2B multiple cloning site

<400> 191

Asn	Ser	Arg	Pro	His	Ser	Arg	Tyr	Leu	Asp	Pro	Ala	Phe	Leu	Tyr	Lys
1				5					10					15	

<210> 192

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR3C multiple cloning site

<220>

<221> CDS

<222> (1)..(63)

<223>

<400> 192

ttg	tac	aaa	aaa	gca	ggc	tct	tta	aag	gaa	cca	att	cag	tcg	act	gga	48
Leu	Tyr	Lys	Lys	Ala	Gly	Ser	Leu	Lys	Glu	Pro	Ile	Gln	Ser	Thr	Gly	
1				5					10					15		

tcc	ggt	acc	gaa	ttc	gatcgc	69
Ser	Gly	Thr	Glu	Phe		
			20			

<210> 193

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR3C multiple cloning site

<400> 193

Leu Tyr Lys Lys Ala Gly Ser Leu Lys Glu Pro Ile Gln Ser Thr Gly
1 5 10 15

Ser Gly Thr Glu Phe
20

<210> 194

<211> 50

<212> DNA

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<220>

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<222> (2)..(49)

<223>

<400> 194

g aat tcg cgg ccg cac tcg aga tat cta gac cca gct ttc ttg tac aaa 49
Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1 5 10 15

g 50

<210> 195

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR3C multiple cloning site

<400> 195

Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1 5 10 15

<210> 196

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR4 multiple cloning site

<220>

<221> CDS

<222> (1)..(63)

<223>

<400> 196

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Leu	Tyr	Lys	Lys	Ala	Gly	Ser	Thr	Met	Gly	Thr	Asn	Ser	Val	Asp	Trp	
1				5					10					15		

atc	cgg	tac	cga	att	c	64
Ile	Arg	Tyr	Arg	Ile		
			20			

<210> 197

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR4 multiple cloning site

<400> 197

Leu	Tyr	Lys	Lys	Ala	Gly	Ser	Thr	Met	Gly	Thr	Asn	Ser	Val	Asp	Trp
1				5					10					15	

Ile	Arg	Tyr	Arg	Ile
			20	

<210> 198

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR4 multiple cloning site

<220>

<221> CDS

<222> (2)..(49)

<223>

<400> 198

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	Asn	Ser	Arg	Pro	His	Ser	Arg	Tyr	Leu	Asp	Pro	Ala	Phe	Leu	Tyr	Lys	
1					5				10					15			

g																	50
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<210> 199

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR4 multiple cloning site

<400> 199

Asn	Ser	Arg	Pro	His	Ser	Arg	Tyr	Leu	Asp	Pro	Ala	Phe	Leu	Tyr	Lys
1				5				10					15		

<210> 200

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR5 multiple cloning site

<220>

<221> CDS

<222> (1)..(63)

<223>

<400> 200

ttg	tac	aaa	aaa	gca	ggc	ttt	cat	atg	gga	acc	aat	tca	gtc	gac	tgg	48
Leu	Tyr	Lys	Lys	Ala	Gly	Phe	His	Met	Gly	Thr	Asn	Ser	Val	Asp	Trp	
1				5					10					15		

atc	cgg	tac	cga	att	cgc	66
Ile	Arg	Tyr	Arg	Ile		
			20			

<210> 201

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR5 multiple cloning site

<400> 201

Leu	Tyr	Lys	Lys	Ala	Gly	Phe	His	Met	Gly	Thr	Asn	Ser	Val	Asp	Trp
1				5					10					15	

Ile	Arg	Tyr	Arg	Ile
			20	

<210> 202

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR5 multiple cloning site

<400> 202

agaattcgcg	gccgcactcg	agatatctag	accagcttt	cttgtaaaa	g	51
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<210> 203

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR6 multiple cloning site

<220>

<221> CDS

<222> (1)..(60)

<223>

<400> 203

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Leu	Tyr	Lys	Lys	Ala	Gly	Cys	Met	Arg	Thr	Asn	Ser	Val	Asp	Trp	Ile	
1				5				10						15		

cgg	tac	cga	att	cgc												63
Arg	Tyr	Arg	Ile													
			20													

<210> 204

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR6 multiple cloning site

<400> 204

Leu	Tyr	Lys	Lys	Ala	Gly	Cys	Met	Arg	Thr	Asn	Ser	Val	Asp	Trp	Ile
1				5				10						15	

Arg	Tyr	Arg	Ile												
			20												

<210> 205

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR6 multiple cloning site

<400> 205

agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g 51

<210> 206

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR7 multiple cloning site

<220>

<221> CDS

<222> (1)..(81)

<223>

<400> 206

ttg tac aaa aaa gca ggc ttt gaa aac ctg tat ttt caa gga acc gtt 48
Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly Thr Val
1 5 10 15

tca tgc atc gtc gac tgg atc cgg tac cga att cgc 84
Ser Cys Ile Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 207

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR7 multiple cloning site

<400> 207

Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly Thr Val
1 5 10 15

Ser Cys Ile Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 208

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR7 multiple cloning site

<400> 208

agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g

51

<210> 209

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR8 multiple cloning site

<220>

<221> CDS

<222> (1)..(78)

<223>

<400> 209

ttg tac aaa aaa gca ggc ttt gaa aac ctg tat ttt caa gga acc atg
Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly Thr Met
1 5 10 15

48

gac cta gtc gac tgg atc cgg tac cga att cgc
Asp Leu Val Asp Trp Ile Arg Tyr Arg Ile
20 25

81

<210> 210

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR8 multiple cloning site

<400> 210

Leu	Tyr	Lys	Lys	Ala	Gly	Phe	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Thr	Met
1				5					10					15	

Asp	Leu	Val	Asp	Trp	Ile	Arg	Tyr	Arg	Ile
			20					25	

<210> 211

<211> 51

<212> DNA

<213> Artifical Sequence

<400> 211

agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g

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<210> 212

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR9 multiple cloning site

<220>

<221> CDS

<222> (1)..(78)

<223>

<400> 212
 ttg tac aaa aaa gca ggc ttt gaa aac ctg tat ttt caa gga cat atg 48
 Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly His Met
 1 5 10 15

aga tct gtc gac tgg atc cgg tac cga att cgc 81
 Arg Ser Val Asp Trp Ile Arg Tyr Arg Ile
 20 25

<210> 213

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR9 multiple cloning site

<400> 213

Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly His Met
 1 5 10 15

Arg Ser Val Asp Trp Ile Arg Tyr Arg Ile
 20 25

<210> 214

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR9 multiple cloning site

<400> 214
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<210> 215

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR10 multiple cloning site

<220>

<221> CDS

<222> (1)..(81)

<223>

<400> 215

ttg	tac	aaa	aaa	gca	ggc	ttc	gaa	cta	agg	aaa	tac	tta	cat	atg	gga	48
Leu	Tyr	Lys	Lys	Ala	Gly	Phe	Glu	Leu	Arg	Lys	Tyr	Leu	His	Met	Gly	
1				5				10						15		

acc	aat	tca	gtc	gac	tgg	atc	cgg	tac	cga	att	cgc	84
Thr	Asn	Ser	Val	Asp	Trp	Ile	Arg	Tyr	Arg	Ile		
			20				25					

<210> 216

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR10 multiple cloning site

<400> 216

Leu	Tyr	Lys	Lys	Ala	Gly	Phe	Glu	Leu	Arg	Lys	Tyr	Leu	His	Met	Gly
1				5				10						15	

Thr	Asn	Ser	Val	Asp	Trp	Ile	Arg	Tyr	Arg	Ile
			20				25			

<210> 217

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR10 multiple cloning site

<400> 217
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<210> 218

<211> 88

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<220>

<221> CDS

<222> (1)..(87)

<223>

<400> 218
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Leu Tyr Lys Lys Ala Gly Phe Glu Gly Asp Arg Thr Asn Ser Leu Arg
1 5 10 15

aaa tac tta acc atg gtc gac tgg atc cgg tac cga att c 88
Lys Tyr Leu Thr Met Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 219

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<400> 219

Leu Tyr Lys Lys Ala Gly Phe Glu Gly Asp Arg Thr Asn Ser Leu Arg
1 5 10 15

Lys Tyr Leu Thr Met Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 220

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<220>

<221> CDS

<222> (2)..(49)

<223>

<400> 220

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	Asn	Ser	Arg	Pro	His	Ser	Arg	Tyr	Leu	Asp	Pro	Ala	Phe	Leu	Tyr	Lys	
1					5				10					15			

g																	50
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<210> 221

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<400> 221

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<210> 222

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<212> DNA

<213> Artificial Sequence

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<223> pDEST1

<400> 222

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aatttcacac aggaaacaga caggtatagg atcacaagtt tgtacaaaaa agctgaacga 120

<210> 223

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST2

<220>

<221> CDS

<222> (94)..(135)

<223>

<400> 223

aatattctga aatgagctgt tgacaattaa tcatccggctc cgtataatct gtggaattgt 60

gagcggataa caatttcaca caggaaacag acc atg tcg tac tac cat cac cat 114
Met Ser Tyr Tyr His His His
1 5

cac cat cac ggc atc aca agt ttgtacaaaa aagctgaa 153
His His His Gly Ile Thr Ser
10

<210> 224

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST2

<400> 224

Met Ser Tyr Tyr His His His His His His Gly Ile Thr Ser
1 5 10

<210> 225

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST3

<220>

<221> CDS

<222> (106)..(120)

<223>

<400> 225

cggttcttggc aaatattctg aaatgagctg ttgacaatta atcatcggct cgtataatgt 60

gtggaattgt gagcggataa caatttcaca caggaaacag tattc atg tcc cct ata 117
Met Ser Pro Ile
1

cta ggttattgga aaattaaggg ccttgtgcaa ccc 153
Leu
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<210> 226

<211> 5

<212> PRT

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<223> pDEST3

<400> 226

Met Ser Pro Ile Leu
1 5

<210> 227

<211> 102

<212> DNA

<213> Artificial Sequence

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<222> (10) .. (63)

<223>

<400> 227

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Arg Gly Ser Arg Arg Ala Ser Val Gly Ser Pro Ser Thr Ser
1 5 10

ttg tac aaa aaa gctgaacgag aaacgtaaaa tgatataaat atcaatata 102
Leu Tyr Lys Lys
15

<210> 228

<211> 18

<212> PRT

<213> Artificial Sequence

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<223> pDEST3

<400> 228

Arg Gly Ser Arg Arg Ala Ser Val Gly Ser Pro Ser Thr Ser Leu Tyr
1 5 10 15

Lys Lys

<210> 229

<211> 255

<212> DNA

<213> Artificial Sequence

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<222> (97)..(246)

<223>

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tgtgagcggg taacaatttc acacaggaaa cagacc atg ggt cat cat cat cat 114
Met Gly His His His His
1 5
cat cac gat tac gat atc cca acg acc gaa aac ctg tat ttt cag ggc 162
His His Asp Tyr Asp Ile Pro Thr Thr Glu Asn Leu Tyr Phe Gln Gly
10 15 20
gcc cat atg agc gat aaa att att cac ctg act gac gac agt gat gac 210
Ala His Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Asp Asp
25 30 35
gat gac aag gta ccc atc aca agt ttg tac aaa aaa gctgaacga 255
Asp Asp Lys Val Pro Ile Thr Ser Leu Tyr Lys Lys
40 45 50

<210> 230

<211> 50

<212> PRT

<213> Artificial Sequence

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<223> pDEST4

<400> 230

Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr Glu
1 5 10 15
Asn Leu Tyr Phe Gln Gly Ala His Met Ser Asp Lys Ile Ile His Leu
20 25 30

Thr Asp Asp Ser Asp Asp Asp Asp Lys Val Pro Ile Thr Ser Leu Tyr
35 40 45

Lys Lys
50

<210> 231

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST5

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gataacaatt tcacacagga aacagctatg accatgatta cgccaagctc taatacgact 120
cactataggg aaagctggta cgcttgcagg taccgggtccg gaattcccgg gtcgacgac 180
acaagtttgt acaaaaaagc tgaa 204

<210> 232

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST5

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agaggatcca agcttacgta cgcggtgcatg cgacgtcata gctcttctat agtgtcacct 120
aaattcaatt cactggccgt cgttttacaa cgtcgtgact gggaaaaccc tggcgttacc 180
caacttaatc gccttgcagc acat 204

<210> 233

<211> 204

<212> DNA

<213> Artificial Sequence

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<223> pDEST6

<400> 233

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gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagcttg gatcctctag	120
agcggccgcc gactagtgat cacaagtttg tacaaaaaag ctgaacgaga aacgtaaaat	180
gatataaata tcaatatatt aaat	204

<210> 234

<211> 255

<212> DNA

<213> Artificial Sequence

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<223> pDEST6

<400> 234

tatttatatc attttacgtt tctcgttcag ctttcttgta caaagtgggtg atcgtcgacc	60
cggggaattcc ggaccggtac ctgcaggcgt accagctttc cctatagtga gtcgtattag	120
agcttggcgt aatcatggtc atagctgttt cctgtgtgaa attgttatcc gtcacaatt	180
ccacacaaca tacgagccgg aagcataaag tgtaaagcct ggggtgccta atgagtgagc	240
taactcacat taatt	255

<210> 235

<211> 306

<212> DNA

<213> Artificial Sequence

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<223> pDEST7

<400> 235

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ttagtgaacc gtcagatcgc ctggagacgc catccacgct gttttgacct ccatagaaga	120

caccgggacc gatccagcct ccggactcta gcctaggccg cggagcggat aacaatttca 180
cacaggaaac agctatgacc actaggcttt tgcaaaaagc tatttaggtg acactataga 240
aggtacgcct gcagggtaccg gtccggaatt cccatcacaa gtttgtacaa aaaagctgaa 300
cgagaa 306

<210> 236

<211> 204

<212> DNA

<213> Artificial Sequence

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<223> pDEST8

<400> 236
cgtatactcc ggaatattaa tagatcatgg agataattaa aatgataacc atctcgcaaa 60
taaataagta ttttactgtt ttcgtaacag ttttgtaata aaaaaaccta taaatattcc 120
ggattattca taccgtecca ccatcgggcg cggatcatca caagtttgta caaaaaagct 180
gaacgagaaa cgtaaaatga tata 204

<210> 237

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST9

<400> 237
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ggtcctagat tgggtgcgta atacacagaa ttctgattgg atcccgggtcc gaagcgcgct 120
ttcccatcaa caagtttgta caaaaaagct gaa 153

<210> 238

<211> 204

<212> DNA

<213> Artificial Sequence

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<220>

<221> CDS

<222> (109)..(201)

<223>

<400> 238

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gattattcat accgtccac catcgggcgc ggatctcggt ccgaaacc atg tcg tac 117
Met Ser Tyr
1

tac cat cac cat cac cat cac gat tac gat atc cca acg acc gaa aac 165
Tyr His His His His His Asp Tyr Asp Ile Pro Thr Thr Glu Asn
5 10 15

ctg tat ttt cag ggc atc aca agt ttg tac aaa aaa gct 204
Leu Tyr Phe Gln Gly Ile Thr Ser Leu Tyr Lys Lys
20 25 30

<210> 239

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST10

<400> 239

Met Ser Tyr Tyr His His His His His His Asp Tyr Asp Ile Pro Thr
1 5 10 15

Thr Glu Asn Leu Tyr Phe Gln Gly Ile Thr Ser Leu Tyr Lys Lys
20 25 30

<210> 240

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST11

<400> 240

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accgggaccg atccagcctc cgcgggcccg aattcgagct cggtagccgg ggatcctcta      120
gagtcgaggt cgacggtatc gataagcttg atatcaacaa gtttgtacaa aaaagctgaa      180
cgagaaacgt aaaatgatat aaat                                             204
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<210> 241

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST12.2

<400> 241

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accgtcagat cgcctggaga cgccatccac gctgttttga cctccataga agacaccggg      60
accgatccag cctccggact ctagcctagg ccgoggagcg gataacaatt tcacacagga      120
aacagctatg accattaggc ctttgcaaaa agctattttag gtgacactat agaaggtacg      180
cctgcaggta ccggtccgga attcccatca acaagtttgt acaaaaaagc tgaacgagaa      240
acgtaaaatg atata                                                         255
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<210> 242

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST13

<400> 242

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tgggcaaacc aagacagcta aagatctctc acctaccaa caatgcccc ctgcaaaaaa      60
taaattcata taaaaaacat acagataacc atctgcggtg ataaattatc tctggcggtg      120
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ttgacataaa taccactggc ggtgatactg agcacatcag caggacgcac tgaccaccat 180
gaaggtgacg ctcttaaaaa ttaagccctg aagaagggca gcattcaaag cagaaggctt 240
tggggtgtgt gatacgaaac gaagcattgg gatcatcaca agtttgtaca aaaaagctga 300

<210> 243

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST14

<400> 243

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actcactata gggagaccac aacggtttcc ctctagatca caagtttgta caaaaaagct 120

<210> 244

<211> 204

<212> DNA

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<223> may be any nucleotide

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<221> CDS

<222> (106)..(120)

<223>

<400> 244

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ccctctagaa ataattttgt ttaactttta gaaggagata tacat atg tcc cct ata 117
Met Ser Pro Ile
1
cta ggttattgga aaattaaggg ccttggtgcaa cccactcgac ttcttttgga 170
Leu
5
atatcttgaa gaaaaatatg aagagcattt gtat 204

<210> 245

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST15

<220>

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<222> (1)..(1)

<223> may be any nucleotide

<400> 245

Met Ser Pro Ile Leu
1 5

<210> 246

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

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<220>

<221> CDS

<222> (70)..(99)

<223>

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cgtccatgg tcg aat caa aca agt ttg tac aaa aaa gct gaacgagaaa      109
      Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
      1              5              10
cgtaaaatga tataaatatc aatatattaa attagatttt gcat      153

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<210> 247

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST15

<400> 247

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Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1              5              10

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<210> 248

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<220>

<221> CDS

<222> (100)..(111)

<223>

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<400> 248
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agaaataatt ttgtttaact ttaagaagga gatatacat atg agc gat aaa      111
      Met Ser Asp Lys
      1

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attatttcacc tgactgacga cagttttgac acggatgtac tc 153

<210> 249

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<400> 249

Met Ser Asp Lys

1

<210> 250

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<220>

<221> CDS

<222> (82)..(123)

<223>

<400> 250

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aacctggccg gttctgggtc t ggt gat gac gat gac aag atc aca agt ttg 111

Gly Asp Asp Asp Asp Lys Ile Thr Ser Leu
1 5 10

tac aaa aaa gct gaacgagaaa cgtaaaatga tataaatatc 153

Tyr Lys Lys Ala

<210> 251

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<400> 251

Gly Asp Asp Asp Asp Lys Ile Thr Ser Leu Tyr Lys Lys Ala
1 5 10

<210> 252

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST17 multiple cloning site

<220>

<221> CDS

<222> (94)..(153)

<223>

<400> 252

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aattttgttt aactttaaga aggagatata cat atg tcg tac tac cat cac cat 114
Met Ser Tyr Tyr His His His
1 5

cac cat cac ctc gaa tca aca agt ttg tac aaa aaa gct 153
His His His Leu Glu Ser Thr Ser Leu Tyr Lys Lys Ala
10 15 20

<210> 253

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST17 multiple cloning site

<400> 253

Met	Ser	Tyr	Tyr	His	His	His	His	His	His	Leu	Glu	Ser	Thr	Ser	Leu
1				5					10					15	

Tyr	Lys	Lys	Ala
			20

<210> 254

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST18 p10 Promoter

<400> 254

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tcctcggttt tctggaaggc gagcatcggt tgttcgcccc ggactctagc tatagttcta	120
gtgggttggt acgtatcgag caagaaaata aaacgccaaa cgcgttgagg tcttgtgtgc	180
tatttttaca aagattcaga aatacgcac acttacaaca aggggggacta tgaaattatg	240
cattttgagg atgccgggac ctttaattca acccaacaca atatattata gttaaataag	300
aattatttat caaatcattt gtatattaat taaaatacta tactgtaaat tacattttat	360
ttacaatgag gatcatcaca agtttgtaca aaaaagctga acgagaaacg taaaatgata	420

<210> 255

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST19 39K Promoter

<400> 255

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aaaaaacccg ccagtttctt ccacaaactc gcgcacggct gtctcgtaaa cttttgcgtc	120

gcaacaatcg cgatgacctc gtggtatgga aatTTTTTct aaaaaagtgt cgttcatgtc 180
ggcgggcgcg ttcgcgctcc ggtacgcgcg acgggcacac agcaggacag cttgtccgg 240
ctcgattatc ataaacaatc ctgcaggcat gcaagctgga tcatcacaag tttgtacaaa 300

<210> 256

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST20 Polyhedron Promoter

<220>

<221> CDS

<222> (163)..(174)

<223>

<400> 256
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gcaaataaat aagtatttta ctgttttcgt aacagttttg taataaaaaa acctataaat 120
attccggatt attcataccg tcccaccatc gggcgcggat cc atg gcc cct ata 174
Met Ala Pro Ile
1
ctaggttatt ggaaaattaa gggccttgtg 204

<210> 257

<211> 4

<212> PRT

<213> Artificial Sequence

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<223> pDEST20 Polyhedron Promoter

<400> 257

Met Ala Pro Ile
1

<210> 258

<211> 95

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST20 Polyhedron Promoter

<220>

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<222> (1)..(48)

<223>

<400> 258

tcg gat ctg gtt ccg cgt cat aat caa aca agt ttg tac aaa aaa gct	48
Ser Asp Leu Val Pro Arg His Asn Gln Thr Ser Leu Tyr Lys Lys Ala	
1 5 10 15	

gaacgagaaaa cgtaaaatga tataaatatc aatatattaa attagat	95
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<210> 259

<211> 16

<212> PRT

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<220>

<223> pDEST20 Polyhedron Promoter

<400> 259

Ser Asp Leu Val Pro Arg His Asn Gln Thr Ser Leu Tyr Lys Lys Ala	
1 5 10 15	

<210> 260

<211> 204

<212> DNA

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<220>

<221> CDS

<222> (163)..(180)

<223>

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agcatacaat caactccaag cttgaagcaa gcctcctgaa ag atg aag cta ctg 174
Met Lys Leu Leu
1
tct tct atcgaacaag catgcatat ttgc 204
Ser Ser
5

<210> 261

<211> 6

<212> PRT

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<220>

<223> pDEST21 Promoter region

<400> 261

Met Lys Leu Leu Ser Ser
1 5

<210> 262

<211> 102

<212> DNA

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<220>

<223> pDEST21 Promoter region

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<222> (37)..(78)

<223>

<400> 262

gaagagagta gtaacaaagg tcaaagacag ttgact gta tcg tcg agg tcg aat	54
Val Ser Ser Arg Ser Asn	
1 5	

caa aca agt ttg tac aaa aaa gct gaacgagaaa cgtaaaatga tata	102
Gln Thr Ser Leu Tyr Lys Lys Ala	
10	

<210> 263

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST21 Promoter region

<400> 263

Val Ser Ser Arg Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1 5 10

<210> 264

<211> 255

<212> DNA

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<223> pDEST22 Promoter region

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aaataaaaaa agtttgccgc tttgctatca agtataaata gacctgcaat tattaatctt 120
ttgtttcctc gtcattgttc tcgttccctt tcttccttgt ttctttttct gcacaatatt 180
tcaagctata ccaagcatatc aatcaactcc aagctt atg ccc aag aag 228
Met Pro Lys Lys
1
aagcggaagg tctcgagcgg cgccaat 255

<210> 265

<211> 4

<212> PRT

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<223> pDEST22 Promoter region

<400> 265

Met Pro Lys Lys
1

<210> 266

<211> 82

<212> DNA

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<220>

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<222> (28)..(66)

<223>

<400> 266
gaagataccc caccaaacc aaaaaaa gag ggt ggg tcg aat caa aca agt ttg 54
Glu Gly Gly Ser Asn Gln Thr Ser Leu

1

5

tac aaa aaa gct gaacgagaaa cgtaaa
Tyr Lys Lys Ala
10

82

<210> 267

<211> 13

<212> PRT

<213> Artificial Sequence

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<223> pDEST22

<400> 267

Glu Gly Gly Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1 5 10

<210> 268

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST23 T7 promoter

<400> 268

atcccgcgaa attaatacga ctactatag ggagaccaca acggtttccc tctagatcac 60

aagtttgtac aaaaaagctg aacgagaaac gtaaaatgat at 102

<210> 269

<211> 153

<212> DNA

<213> Artificial Sequence

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<223> pDEST23 T7 promoter

<220>

<221> CDS

<222> (61)..(126)

<223>

<400> 269

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gct ttc ttg tac aaa gtg gtg att atg tcg tac tac cat cac cat cac 108

Ala Phe Leu Tyr Lys Val Val Ile Met Ser Tyr Tyr His His His His
1 5 10 15

cat cac ctc gat gag caa taactagcat aaccccttgg ggcctct 153

His His Leu Asp Glu Gln
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<210> 270

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST23 T7 promoter

<400> 270

Ala Phe Leu Tyr Lys Val Val Ile Met Ser Tyr Tyr His His His His
1 5 10 15

His His Leu Asp Glu Gln
20

<210> 271

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST24 T7 promoter

<400> 271

atcgagatct cgatcccgcg aaattaatac gactcactat agggagacca caacggtttc 60

cctctagatc acaagtttgc acaaaaaagc tgaacgagaa ac 102

<210> 272

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST24 T7 promoter

<220>

<221> CDS

<222> (22)..(60)

<223>

<400> 272

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			Ala	Phe	Leu	Tyr	Lys	Val	Val	Ile	Met	Ser	
			1				5					10	

cct	ata	cta	ggttattgga	aaattaaggg	ccttggtgcaa	cccactcgac	tt	102
Pro	Ile	Leu						

<210> 273

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST24 T7 promoter

<400> 273

Ala	Phe	Leu	Tyr	Lys	Val	Val	Ile	Met	Ser	Pro	Ile	Leu
1				5					10			

<210> 274

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST25 T7 promoter

<220>

<221> misc_feature

<222> (1)..(1)

<223> May be any nucleotide

<400> 274

nagatctcga tcccgcgaaa ttaatacgac tcactatagg gagaccacaa cggtttcct 60

ctagatcaca agtttgtaca aaaaagctga acgagaaacg ta 102

<210> 275

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST25 T7 promoter

<220>

<221> CDS

<222> (19)..(60)

<223>

<400> 275

ttttacgttt ctcgttca gct ttc ttg tac aaa gtg gtg att atg agc gat 51

Ala Phe Leu Tyr Lys Val Val Ile Met Ser Asp
1 5 10

aaa att att cacctgactg acgacagttt tgacacggat gtactcaaag cg 102
Lys Ile Ile

<210> 276

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST25 T7 promoter

<400> 276

Ala Phe Leu Tyr Lys Val Val Ile Met Ser Asp Lys Ile Ile
1 5 10

<210> 277

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST26 CMV promoter

<220>

<221> CDS

<222> (238)..(297)

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acaactccgc cccattgacg caaatgggag gtaggcgtgt acggtgggag gtctatataa 120
gcagagctcg tttagtgaac cgtcagatcg cctggagacg ccatccacgc tgttttgacc 180
tccatagaag acaccgggac cgatccagcc tccggactct agcctaggcc gcggacc 237
atg gcg tac tac cat cac cat cac cat cac tct aga tca aca agt ttg 285
Met Ala Tyr Tyr His His His His His His Ser Arg Ser Thr Ser Leu
1 5 10 15
tac aaa aaa gct gaacgagaa 306
Tyr Lys Lys Ala
20

<210> 278

<211> 20

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<213> Artificial Sequence

<220>

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<400> 278

Met	Ala	Tyr	Tyr	His	His	His	His	His	His	Ser	Arg	Ser	Thr	Ser	Leu
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Tyr	Lys	Lys	Ala
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tagcctaggc cgcggacc atg gcc cct ata cta ggttattgga aaattaaggg	173
Met Ala Pro Ile Leu	
1 5	
ccttgtgcaa cccactcgac ttcttttgga atatcttgaa gaaaaatatg aagagcattt	233

gtatgagcgc gatgaaggatg at

255

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Met Ala Pro Ile Leu
1 5

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Val Pro Arg Ser Arg Ser
1 5

aca agt ttg tac aaa aaa gct gaacgagaaa cg 87
Thr Ser Leu Tyr Lys Lys Ala

10

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Val	Pro	Arg	Ser	Arg	Ser	Thr	Ser	Leu	Tyr	Lys	Lys	Ala
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<212> DNA

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acaatttcac acaggaaaca gctatgacca ttaggcctat ttaggtgaca ctatagaaca	180
agtttgtaca aaaaagcagg ctggtaccgg tccggaattc ccgggatatc gtcgacgagc	240
tcactagtcg gcggccgctc tagagtatcc ctcgaggggc ccaagcttac gcgtacccag	300
ctttcttgta caaagtggtc cctatagtga gtcgtattat aagctaggca ctggccgctc	360
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Met Ser Tyr Tyr His His His His
1 5

cat cac ggc atc aca agt ttg tac aaa aaa gca ggc ttt gaa aac ctg 102
His His Gly Ile Thr Ser Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu
10 15 20

tat ttt caa gga acc atg gag aaa aaa atc act gga tat acc acc gtt 150
Tyr Phe Gln Gly Thr Met Glu Lys Lys Ile Thr Gly Tyr Thr Thr Val
25 30 35 40

gat 153
Asp

<210> 285

<211> 41

<212> PRT

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<223> His6-CAT

<400> 285

Met Ser Tyr Tyr His His His His His His Gly Ile Thr Ser Leu Tyr
1 5 10 15

Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly Thr Met Glu Lys
20 25 30

Lys Ile Thr Gly Tyr Thr Thr Val Asp
35 40